Serial Number: O9 852,922

CRF Processing Date: _____
Edited by: _____
Verified by: _____ (STIC sta

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line. #2

☐ Edited a format error in the Current Application Data section, specifically **ENTERED**

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☑ Deleted: ☑ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file. ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/852,922

DATE: 06/21/2001
TIME: 10:22:29

Input Set : A:\Cpg.pto
Output Set: N:\CRF3\06202001\I852922.raw

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 2 <110> APPLICANT: TOYO BOSEKI KABUSHIKI KAISHA
 4 <120> TITLE OF INVENTION: MODIFIED THERMOSTABLE DNA POLYMERASE
 6 <130> FILE REFERENCE: 000053
 8 <140> CURRENT APPLICATION NUMBER: US/09/852,922
 9 <141> CURRENT FILING DATE: 2001-05-10
11 <150> PRIOR APPLICATION NUMBER: 2000-138796
12 <151> PRIOR FILING DATE: 2000-05-11
14 <160> NUMBER OF SEQ ID NOS: 28
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 5342
20 <212> TYPE: DNA
21 <213> ORGANISM: Pyrococcus kodakaraensis
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (156)..(5165)
26 <223> OTHER INFORMATION: 1374-2453 intron, 2709-4316 intron
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33 cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac     173
34                                         Met Ile Leu Asp Thr Asp
35                                         1               5
37 tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221
38 Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu
39                 10              15                  20
41 aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269
42 Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe
43             25              30                  35
45 tac gcc ctc ctg aag gac gat tct gcc att gag gaa gtc aag aag ata 317
46 Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile
47         40              45                  50
49 acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365
50 Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys
51 55              60                  65                  70
53 gtt cag aag aag ttc ctc ggg aga cca gtt gag gtc tgg aaa ctc tac 413
54 Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr
55                 75              80                  85
57 ttt act cat ccg cag gac gtc cca gcg ata agg gac aag ata cga gag 461
58 Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu
59             90              95                  100
61 cat ggg gca gtt att gac atc tac gag tac gac ata ccc ttc gcc aag 509
62 His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys
63             105             110                 115
65 cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag 557
66 Arg Tyr Leu Ile Asp Lys Gly Leu Val Pro Met Glu Gly Asp Glu Glu
67     120             125             130
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6/21/01

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69  ctg aaa atg ctc gcc ttc gac att gaa act ctc tac cat gag ggc gag      605
70  Leu Lys Met Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu
71  135                     140                 145                 150
73  gag ttc gcc gag ggg cca atc ctt atg ata agc tac gcc gac gag gaa      653
74  Glu Phe Ala Glu Gly Pro Ile Leu Met Ile Ser Tyr Ala Asp Glu Glu
75                          155                 160                 165
77  ggg gcc agg gtg ata act tgg aag aac gtg gat ctc ccc tac gtt gac      701
78  Gly Ala Arg Val Ile Thr Trp Lys Asn Val Asp Leu Pro Tyr Val Asp
79                  170                 175                 180
81  gtc gtc tcg acg gag agg gag atg ata aag cgc ttc ctc cgt gtt gtg      749
82  Val Val Ser Thr Glu Arg Glu Met Ile Lys Arg Phe Leu Arg Val Val
83              185                 190                 195
85  aag gag aaa gac ccg gac gtt ctc ata acc tac aac ggc gac aac ttc      797
86  Lys Glu Lys Asp Pro Asp Val Leu Ile Thr Tyr Asn Gly Asp Asn Phe
87      200                 205                 210
89  gac ttc gcc tat ctg aaa aag cgc tgt gaa aag ctc gga ata aac ttc      845
90  Asp Phe Ala Tyr Leu Lys Lys Arg Cys Glu Lys Leu Gly Ile Asn Phe
91  215                 220                 225                 230
93  gcc ctc gga agg gat gga agc gag ccg aag att cag agg atg ggc gac      893
94  Ala Leu Gly Arg Asp Gly Ser Glu Pro Lys Ile Gln Arg Met Gly Asp
95                  235                 240                 245
97  agg ttt gcc gtc gaa gtg aag gga cgg ata cac ttc gat ctc tat cct      941
98  Arg Phe Ala Val Glu Val Lys Gly Arg Ile His Phe Asp Leu Tyr Pro
99                  250                 255                 .260
101 gtg ata aga cgg acg ata aac ctg ccc aca tac acg ctt gag gcc gtt      989
102 Val Ile Arg Arg Thr Ile Asn Leu Pro Thr Tyr Thr Leu Glu Ala Val
103             265                 270                 275       .
105 tat gaa gcc gtc ttc ggt cag ccg aag gag aag gtt tac gct gag gaa      1037
106 Tyr Glu Ala Val Phe Gly Gln Pro Lys Glu Lys Val Tyr Ala Glu Glu
107     280                 285                 290
109 ata acc aca gcc tgg gaa acc ggc gag aac ctt gag aga gtc gcc cgc      1085
110 Ile Thr Thr Ala Trp Glu Thr Gly Glu Asn Leu Glu Arg Val Ala Arg
111 295                 300                 305                 310
113 tac tcg atg gaa gat gcg aag gtc aca tac gag ctt ggg aag gag ttc      1133
114 Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr Glu Leu Gly Lys Glu Phe
115                 315                 320                 325
117 ctt ccg atg gag gcc cag ctt tct cgc tta atc ggc cag tcc ctc tgg      1181
118 Leu Pro Met Glu Ala Gln Leu Ser Arg Leu Ile Gly Gln Ser Leu Trp
119             330                 335                 340
121 gac gtc tcc cgc tcc agc act ggc aac ctc gtt gag tgg ttc ctc ctc      1229
122 Asp Val Ser Arg Ser Ser Thr Gly Asn Leu Val Glu Trp Phe Leu Leu
123             345                 350                 355
125 agg aag gcc tat gag agg aat gag ctg gcc ccg aac aag ccc gat gaa      1277
126 Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala Pro Asn Lys Pro Asp Glu
127     360                 365                 370
129 aag gag ctg gcc aga aga cgg cag agc tat gaa gga ggc tat gta aaa      1325
130 Lys Glu Leu Ala Arg Arg Arg Gln Ser Tyr Glu Gly Gly Tyr Val Lys
131 375                 380                 385                 390
133 gag ccc gag aga ggg ttg tgg gag aac ata gtg tac cta gat ttt aga      1373
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134 Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile Val Tyr Leu Asp Phe Arg
135                 395             400             ·       405
137 tgc cat cca gcc gat acg aag gtt gtc gtc aag ggg aag ggg att ata    1421
138 Cys His Pro Ala Asp Thr Lys Val Val Val Lys Gly Lys Gly Ile Ile
139             410             415                     420
141 aac atc agc gag gtt cag gaa ggt gac tat gtc ctt ggg att gac ggc    1469
142 Asn Ile Ser Glu Val Gln Glu Gly Asp Tyr Val Leu Gly Ile Asp Gly
143         425             430             ·       435
145 tgg cag aga gtt aga aaa gta tgg gaa tac gac tac aaa ggg gag ctt    1517
146 Trp Gln Arg Val Arg Lys Val Trp Glu Tyr Asp Tyr Lys Gly Glu Leu
147     440             445             450
149 gta aac ata aac ggg tta aag tgt acg ccc aat cat aag ctt ccc gtt    1565
150 Val Asn Ile Asn Gly Leu Lys Cys Thr Pro Asn His Lys Leu Pro Val
151 455             460             465                     470
153 gtt aca aag aac gaa cga caa acg aga ata aga gac agt ctt gct aag    1613
154 Val Thr Lys Asn Glu Arg Gln Thr Arg Ile Arg Asp Ser Leu Ala Lys
155             475             480             485
157 tct ttc ctt act aaa aaa gtt aag ggc aag ata ata acc act ccc ctt    1661
158 Ser Phe Leu Thr Lys Lys Val Lys Gly Lys Ile Ile Thr Thr Pro Leu
159             490             495             500
161 ttc tat gaa ata ggc aga gcg aca agt gag aat att cca gaa gaa gag    1709
162 Phe Tyr Glu Ile Gly Arg Ala Thr Ser Glu Asn Ile Pro Glu Glu Glu
163         ·       505             510             515
165 gtt ctc aag gga gag ctc gct ggc ata cta ttg gct gaa gga acg ctc    1757
166 Val Leu Lys Gly Glu Leu Ala Gly Ile Leu Leu Ala Glu Gly Thr Leu
167     520             525             530
169 ttg agg aaa gac gtt gaa tac ttt gat tca tcc cgc aaa aaa cgg agg    1805
170 Leu Arg Lys Asp Val Glu Tyr Phe Asp Ser Ser Arg Lys Lys Arg Arg
171 535             540             545                     550
173 att tca cac cag tat cgt gtt gag ata acc att ggg aaa gac gag gag    1853
174 Ile Ser His Gln Tyr Arg Val Glu Ile Thr Ile Gly Lys Asp Glu Glu
175             555             560             565
177 gag ttt agg gat cgt atc aca tac att ttt gag cgt ttg ttt ggg att    1901
178 Glu Phe Arg Asp Arg Ile Thr Tyr Ile Phe Glu Arg Leu Phe Gly Ile
179             570             575             580
181 act cca agc atc tcg gag aag aaa gga act aac gca gta aca ctc aaa    1949
182 Thr Pro Ser Ile Ser Glu Lys Lys Gly Thr Asn Ala Val Thr Leu Lys
183         585             590             595
185 gtt gcg aag aag aat gtt tat ctt aaa gtc aag gaa att atg gac aac    1997
186 Val Ala Lys Lys Asn Val Tyr Leu Lys Val Lys Glu Ile Met Asp Asn
187     600             605             ·       610
189 ata gag tcc cta cat gcc ccc tcg gtt ctc agg gga ttc ttc gaa ggc    2045
190 Ile Glu Ser Leu His Ala Pro Ser Val Leu Arg Gly Phe Phe Glu Gly
191 615             620             625                     630
193 gac ggt tca gta aac agg gtt agg agg agt att gtt gca acc cag ggt    2093
194 Asp Gly Ser Val Asn Arg Val Arg Arg Ser Ile Val Ala Thr Gln Gly
195             635             640             645
197 aca aag aac gag tgg aag att aaa ctg gtg tca aaa ctg ctc tcc cag    2141
198 Thr Lys Asn Glu Trp Lys Ile Lys Leu Val Ser Lys Leu Leu Ser Gln
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199          650                655                660
201 ctt ggt atc cct cat caa acg tac acg tat cag tat cag gaa aat ggg   2189
202 Leu Gly Ile Pro His Gln Thr Tyr Thr Tyr Gln Tyr Gln Glu Asn Gly
203         ·665                670                     675
205 aaa gat cgg agc agg tat ata ctg gag ata act gga aag gac gga ttg   2237
206 Lys Asp Arg Ser Arg Tyr Ile Leu Glu Ile Thr Gly Lys Asp Gly Leu
207     680                685                690
209 ata ctg ttc caa aca ctc att gga ttc atc agt gaa aga aag aac gct   2285
210 Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala
211 695                700                705                     710
213 ctg·ctt aat aag gca ata tct cag agg gaa atg aac aac ttg gaa aac   2333·
214 Leu Leu Asn Lys Ala Ile Ser Gln Arg Glu Met Asn Asn Leu Glu Asn
215                 715                720                     725
217 aat gga ttt tac agg ctc agt gaa ttc aat gtc agc acg gaa tac tat   2381
218 Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr
219             730                735                740
221 gag ggc aag gtc tat gac tta act ctt gaa gga act ccc tac tac ttt   2429
222 Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe
223         745                750                755
225 gcc aat ggc ata ttg acc cat aac tcc ctg tac ccc tca atc atc atc   2477
226 Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile
227     760                765                770
229 acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa   2525
230 Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu
231 775                780                785                     790
233 tat gac gtt gcc cca cag gtc ggc cac cgc ttc tgc aag gac ttc cca   2573
234 Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro
235                 795 ·            800                805
237 gga ttt atc ccg agc ctg ctt gga gac ctc cta gag gag agg cag aag   2621
238 Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys
239             810                815                820
241 ata aag aag aag atg aag gcc acg att gac ccg atc gag agg aag ctc   2669
242 Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu
243         825                830                835
245 ctc gat tac agg cag agg gcc atc aag atc ctg gca aac agc atc cta   2717
246 Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu
247     840                845                     850
249 ccc gag gaa tgg ctt cca gtc ctc gag gaa ggg gag gtt cac·ttc gtc   2765
250 Pro Glu Glu Trp Leu Pro Val Leu Glu Glu Gly Glu Val His Phe Val
251 855                860                865                     870
253 agg att gga gag ctc ata gac cgg atg atg gag gaa aat gct ggg aaa   2813
254 Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys
255             875                880                     885
257 gta aag aga gag ggc gag acg gaa gtg ctt gag gtc agt ggg ctt gaa   2861
258 Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu
259             890                895                900
261 gtc ccg tcc ttt aac agg aga act aac aag gcc gag ctc aag aga gta   2909
262 Val Pro Ser Phe Asn Arg Arg Thr Asn Lys Ala Glu Leu Lys Arg Val
263         905                910                     915
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265 aag gcc ctg att agg cac gat tat tct ggc aag gtc tac acc atc aga    2957
266 Lys Ala Leu Ile Arg His Asp Tyr Ser Gly Lys Val Tyr Thr Ile Arg
267     920                     925                 930
269 ctg aag tcg ggg agg aga ata aag ata acc tct ggc cac agc ctc ttc    3005
270 Leu Lys Ser Gly Arg Arg Ile Lys Ile Thr Ser Gly His Ser Leu Phe
271 935                     940                 945                 950
273 tct gtg aga aac ggg gag ctc gtt gaa gtt acg ggc gat gaa cta aag    3053
274 Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys
275                     955                 960                 965
277 cca ggt gac ctc gtt gca gtc ccg cgg aga ttg gag ctt cct gag aga    3101
278 Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg
279             970                 975                 980
281 aac cac gtg ctg aac ctc gtt gaa ctg ctc ctt gga acg cca gaa gaa    3149
282 Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu
283         985                 990                 995
285 gaa act ttg gac atc gtc atg acg atc cca gtc aag ggt aag aag aac    3197
286 Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn
287     1000                1005                1010
289 ttc ttt aaa ggg atg ctc agg act ttg cgc tgg att ttc gga gag gaa    3245
290 Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu
291 1015                1020                1025                1030
293 aag agg ccc aga acc gcg aga cgc tat ctc agg cac ctt gag gat ctg    3293
294 Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu
295                 1035                1040                1045
297 ggc tat gtc cgg ctt aag aag atc ggc tac gaa gtc ctc gac tgg gac    3341
298 Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp
299             1050                1055                1060
301 tca ctt aag aac tac aga agg ctc tac gag gcg ctt gtc gag aac gtc    3389
302 Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val
303         1065                1070                1075
305 aga tac aac ggc aac aag agg gag tac ctc gtt gaa ttc aat tcc atc    3437
306 Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile
307     1080                1085                1090
309 cgg gat gca gtt ggc ata atg ccc cta aaa gag ctg aag gag tgg aag    3485
310 Arg Asp Ala Val Gly Ile Met Pro Leu Lys Glu Leu Lys Glu Trp Lys
311 1095                1100                1105                1110
313 atc ggc acg ctg aac ggc ttc aga atg aga aag ctc att gaa gtg gac    3533
314 Ile Gly Thr Leu Asn Gly Phe Arg Met Arg Lys Leu Ile Glu Val Asp
315                 1115                1120                . 1125
317 gag tcg tta gca aag ctc ctc ggc tac tac gtg agc gag ggc tat gca    3581
318 Glu Ser Leu Ala Lys Leu Leu Gly Tyr Tyr Val Ser Glu Gly Tyr Ala
319             1130                1135                1140
321 aga aag cag agg aat ccc aaa aac ggc tgg agc tac agc gtg aag ctc    3629
322 Arg Lys Gln Arg Asn Pro Lys Asn Gly Trp Ser Tyr Ser Val Lys Leu
323     1145                1150                1155
325 tac aac gaa gac cct gaa gtg ctg gac gat atg gag aga ctc gcc agc    3677
326 Tyr Asn Glu Asp Pro Glu Val Leu Asp Asp Met Glu Arg Leu Ala Ser
327 1160                1165                1170
329 agg ttt ttc ggg aag gtg agg cgg ggc agg aac tac gtt gag ata ccg    3725
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VERIFICATION SUMMARY   DATE: 06/21/2001
PATENT APPLICATION: US/09/852,922   TIME: 10:22:30

Input Set : **A:\Cpg.pto**
Output Set: **N:\CRF3\06202001\I852922.raw**

L:8 M:270 C: Current Application Number differs, Replaced Application Number
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date